AMENDMENTS TO THE CLAIMS

1. (Currently Amended) A process for analyzing proteins or viruses in a sample comprising:

dividing a sample having a protein or virus component into a plurality of aliquots;

applying said plurality of aliquots in parallel to a plurality of simultaneous ~~different~~ n first separation steps;

washing said first separation steps with a set of monotonically changing buffers C_0 to C_{n-1};

eluting said first separation steps with buffer set C_1 to C_n to yield a plurality of uniquely different partially resolved eluates;

subjecting said plurality of partially resolved eluates in parallel to a second separation step to yield a plurality of resolved fractions, and

analyzing at least one of said plurality of resolved fractions.

2. (Previously Presented) The process of claim 1 further comprising collecting at least one of said plurality of resolved fractions.

3. (Original) The process of claim 2 wherein collection of the at least one of said plurality of resolved fractions occurs onto a MALDI target or plate.

4. (Canceled)

5. (Currently Amended) The process of claim [[4]] 1 wherein analysis is by mass spectrometry.

6. (Original) The process of claim 5 wherein said mass spectrometry is performed on a MALDI mass spectrometer.

7. (Previously Presented) The process of claim 3 further comprising the step of analyzing at least one of said plurality of resolved fractions by mass spectrometry wherein said mass spectrometry is performed on an orthogonal MALDI mass spectrometer.

8. (Original) The process of claim 1 wherein at least one of said first and said second separation steps separate on a basis selected from the group consisting of: charge, molecular weight, and hydrophobicity.

9. (Original) The process of claim 1 wherein at least one of said first and said second separation steps uses a chromatography resin or chromatography membrane.

10. (Original) The process of claim 1 wherein at least one of said first and said second separation steps comprises a separation buffer that varies monotonically between individual aliquots or individual eluates.

11. (Original) The process of claim 1 wherein at least one of said first and said second separation steps comprises a separation matrix in linear or two-dimensional array.

12. (Original) The process of claim 11 wherein said first and said second separation steps occur with matrices maintaining well addresses in each of the two matrices.

13. (Original) The process of claim 1 wherein at least one of said first or said second separation steps occurs within a microplate.

14. (Previously Presented) The process of claim 1 further comprising: digesting said plurality of partially resolved eluates prior to subjecting said plurality of partially resolved eluates in parallel to said second separation step.

15. (Currently Amended) A process for analyzing proteins or viruses in a sample comprising:

dividing a sample having a protein or virus component into a plurality of aliquots;

applying said plurality of aliquots in parallel to a plurality of simultaneous ~~different~~ n first separation steps;

washing said first separation steps with a set of monotonically changing buffers C_0 to C_{n-1};

eluting said first separation steps with buffer set C_1 to C_n to yield a plurality of uniquely different partially resolved eluates;

subjecting said plurality of partially resolved eluates in parallel to a second separation step to yield a plurality of resolved fractions;

digesting said plurality of partially resolved eluates with a proteolytic enzyme to yield a plurality of digested eluates;

subjecting said plurality of digested eluates in parallel to a second separation step to yield a plurality of resolved peptide fractions, and

analyzing at least one of said plurality of resolved fractions.

16. (Previously Presented) The process of claim 15 further comprising: collecting at least one of said plurality of resolved fractions.

17. (Original) The process of claim 16 wherein collection of the at least one of said plurality of resolved fractions occurs onto a MALDI target or plate.

18. (Canceled)

19. (Currently Amended) The process of claim [[18]] 15 wherein analysis is by mass spectrometry.

20. (Canceled)

21. (Original) The process of claim 19 wherein said mass spectrometry is performed on an orthogonal MALDI mass spectrometer.

22. (Original) The process of claim 15 wherein at least one of said first and said second separation steps separate on a basis selected from the group consisting of: charge, molecular weight, and hydrophobicity.

23. (Canceled)

24. (Original) The process of claim 15 wherein at least one of said first and said second separation steps comprises a separation buffer that varies monotonically between individual aliquots or individual eluates.

25. (Original) The process of claim 15 wherein at least one of said first and said second separation steps comprises a separation matrix in linear or two-dimensional array.

26. (Original) The process of claim 25 wherein said first and said second separation steps occur with matrices maintaining well addresses in each of the two matrices.

27. (Original) The process of claim 15 wherein at least one of said first or said second separation steps occurs within a microplate.

28. (Canceled)

29. (Canceled)

30. (Currently Amended) The process of claim [[18]] 15 further comprising analyzing at least one of said plurality of partially resolved eluates prior to digestion in concert with the corresponding resolved fraction.

31. (Original) The process of claim 30 wherein analysis is by mass spectrometry.

32. (Previously Presented) The process of claim 1 wherein the step of applying said plurality of aliquots in parallel to said first separation step is performed by a robot.

33. (Previously Presented) The process of claim 1 further comprising affixing a machine-readable label to at least one collection selected from the group consisting of: said plurality of aliquots, said plurality of partially resolved eluates, and said plurality of resolved fractions.

34. (Previously Presented) The process of claim 1 further comprising the steps of:
labeling a subsample with a unique tag; and
combining said subsample with a second uniquely labeled subsample or an unlabeled subsample prior to said plurality of aliquots.

35-42. (Canceled)